

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Bryan, Bruce
- (ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Heller Ehrman White & McAuliffe
  - (B) STREET: 4250 Executive Square, 7th Floor
  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/757,046
  - (B) FILING DATE: 11-25-96
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/597,274
  - (B) FILING DATE: 02-06-96
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seidman, Stephanie L
  - (B) REGISTRATION NUMBER: 33,779
  - (C) REFERENCE/DOCKET NUMBER: 24727-105C
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619-450-8400
  - (B) TELEFAX: 619-450-8499
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...942

## (D) OTHER INFORMATION: Renilla Reinformis Luciferase

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35					40					45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
	50					55				60						
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65					70				75					80		
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85					90					95		
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
			100					105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
		115					120					125				
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
	130					135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
	145				150					155				160		
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165					170					175		
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
			180					185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624
Ile	Met	Arg	Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro	
		195					200					205				
TTC	AAA	GAG	AAA	GGT	GAA	GTT	CGT	CGT	CCA	ACA	TTA	TCA	TGG	CCT	CGT	672
Phe	Lys	Glu	Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg	
	210					215					220					
GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT	720

Glu	Ile	Pro	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val		
225					230					235					240		
AGG	AAT	TAT	AAT	GCT	TAT	CTA	CGT	GCA	AGT	GAT	GAT	TTA	CCA	AAA	ATG	768	
Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met		
			245					250						255			
TTT	ATT	GAA	TCG	GAT	CCA	GGA	TTC	TTT	TCC	AAT	GCT	ATT	GTT	GAA	GGC	816	
Phe	Ile	Glu	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly		
			260				265						270				
GCC	AAG	AAG	TTT	CCT	AAT	ACT	GAA	TTT	GTC	AAA	GTA	AAA	GGT	CTT	CAT	864	
Ala	Lys	Lys	Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His		
		275					280					285					
TTT	TCG	CAA	GAA	GAT	GCA	CCT	GAT	GAA	ATG	GGA	AAA	TAT	ATC	AAA	TCG	912	
Phe	Ser	Gln	Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Lys	Tyr	Ile	Lys	Ser		
	290					295					300						
TTC	GTT	GAG	CGA	GTT	CTC	AAA	AAT	GAA	CAA	TAA	TTACTTTGGT	TTTTTATTTA				965	
Phe	Val	Glu	Arg	Val	Leu	Lys	Asn	Glu	Gln								
305					310												
CATTTTTC	GGGTTTA	ATAATGT	CATTTTCA	AATTTTAT	TTACTGA											1025	
TTTACAGG	AACATTC	TATGTTG	AATTTAG	CTC	GAACTTT	ACTGTC	ATATC									1085	
ATTTTGGA	ATTACCT	CTT	TCAATGA	AAC	TTTATAA	ACA	GTGGTT	CAAT	TAATTA	ATAT						1145	
ATATTATA	TACATTT	GTT	ATGTAATA	AAA	CTCGGTT	TTA	TTATAAAA	A								1196	

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorffii luciferase

## (x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG	AAG	CTA	ATA	ATT	CTG	TCT	ATT	ATA	TTG	GCC	TAC	TGT	GTC	ACA	GTC	48	
Met	Lys	Leu	Ile	Ile	Leu	Ser	Ile	Ile	Leu	Ala	Tyr	Cys	Val	Thr	Val		
1				5					10					15			
AAC	TGC	CAG	GAT	GCA	TGT	CCT	GTA	GAA	GCT	GAA	GCA	CCG	TCA	AGT	ACA	96	
Asn	Cys	Gln	Asp	Ala	Cys	Pro	Val	Glu	Ala	Glu	Ala	Pro	Ser	Ser	Thr		
			20					25					30				
CCA	ACA	GTC	CCA	ACA	TCT	TGT	GAA	GCT	AAA	GAA	GGA	GAA	TGT	ATC	GAT	144	
Pro	Thr	Val	Pro	Thr	Ser	Cys	Glu	Ala	Lys	Glu	Gly	Glu	Cys	Ile	Asp		
		35					40					45					
ACC	AGA	TGC	GCA	ACA	TGT	AAA	CGA	GAC	ATA	CTA	TCA	GAC	GGA	CTG	TGT	192	
Thr	Arg	Cys	Ala	Thr	Cys	Lys	Arg	Asp	Ile	Leu	Ser	Asp	Gly	Leu	Cys		
	50					55					60						

GAA Glu 65	AAT Asn	AAA Lys	CCA Pro	GGG Gly	AAG Lys 70	ACA Thr	TGC Cys	TGT Cys	AGA Arg	ATG Met 75	TGC Cys	CAG Gln	TAT Tyr	GTA Val	ATT Ile 80	240
GAA Glu	TCC Ser	AGA Arg	GTA Val	GAA Glu 85	GCT Ala	GCT Ala	GGA Gly	TAT Tyr	TTT Phe 90	AGA Arg	ACG Thr	TTT Phe	TAC Tyr	GCC Ala 95	AAA Lys	288
AGA Arg	TTT Phe	AAT Asn	TTT Phe 100	CAG Gln	GAA Glu	CCT Pro	GGT Gly	AAA Lys 105	TAT Tyr	GTG Val	CTG Leu	GCT Ala	CGA Arg 110	GGA Gly	ACC Thr	336
AAG Lys	GGT Gly	GGC Gly 115	GAC Asp	TGG Trp	TCT Ser	GTA Val	ACC Thr 120	CTC Leu	ACC Thr	ATG Met	GAG Glu	AAT Asn 125	CTA Leu	GAT Asp	GGA Gly	384
CAG Gln 130	AAG Lys	GGA Gly	GCT Ala	GTA Val	CTG Leu	ACT Thr 135	AAG Lys	ACA Thr	ACA Thr	CTG Leu 140	GAG Glu	GTA Val	GTA Val	GGA Gly	GAC Asp	432
GTA Val 145	ATA Ile	GAC Asp	ATT Ile	ACT Thr	CAA Gln 150	GCT Ala	ACT Thr	GCA Ala	GAT Asp 155	CCT Pro 155	ATC Ile	ACA Thr	GTT Val	AAC Asn	GGA Gly 160	480
GGA Gly	GCT Ala	GAC Asp	CCA Pro	GTT Val 165	ATC Ile	GCT Ala	AAC Asn	CCG Pro	TTC Phe 170	ACA Thr	ATT Ile	GGT Gly	GAG Glu	GTG Val 175	ACC Thr	528
ATT Ile	GCT Ala	GTT Val 180	GTC Val	GAA Glu	ATA Ile	CCC Pro	GGC Gly	TTC Phe 185	AAT Asn	ATT Ile	ACA Thr	GTC Val	ATC Ile 190	GAA Glu	TTC Phe	576
TTT Phe	AAA Lys	CTA Leu 195	ATC Ile	GTG Val	ATA Ile	GAT Asp	ATT Ile 200	CTG Leu	GGA Gly	GGA Gly	AGA Arg	TCT Ser 205	GTG Val	AGA Arg	ATT Ile	624
GCT Ala 210	CCA Pro	GAC Asp	ACA Thr	GCA Ala	AAC Asn	AAA Lys 215	GGA Gly	CTG Leu	ATA Ile	TCT Ser 220	GGT Gly	ATC Ile	TGT Cys	GGT Gly	AAT Asn	672
CTG Leu 225	GAG Glu	ATG Met	AAT Asn	GAC Asp	GCT Ala 230	GAT Asp	GAC Asp	TTT Phe	ACT Thr	ACA Thr 235	GAC Asp	GCA Ala	GAT Asp	CAG Gln	CTG Leu 240	720
GCG Ala	ATC Ile	CAA Gln	CCC Pro	AAC Asn 245	ATA Ile	AAC Asn	AAA Lys	GAG Glu 250	TTC Phe	GAC Asp 250	GGC Gly	TGC Cys	CCA Pro	TTC Phe 255	TAC Tyr	768
GGG Gly	AAT Asn	CCT Pro	TCT Ser 260	GAT Asp	ATC Ile	GAA Glu	TAC Tyr 265	TGC Cys	AAA Lys	GGT Gly	CTC Leu	ATG Met 270	GAG Glu	CCA Pro	TAC Tyr	816
AGA Arg	GCT Ala	GTA Val 275	TGT Cys	CGT Arg	AAC Asn	AAT Asn	ATC Ile 280	AAC Asn	TTC Phe	TAC Tyr	TAT Tyr 285	TAC Tyr	ACT Thr	CTG Leu	TCC Ser	864
TGC Cys 290	GCC Ala	TTC Phe	GCT Ala	TAC Tyr	TGT Cys	ATG Met 295	GGA Gly	GGA Gly	GAA Glu	GAA Glu	AGA Arg 300	GCT Ala	AAA Lys	CAC His	GTC Val	912
CTT Leu 305	TTC Phe	GAC Asp	TAT Tyr	GTT Val	GAG Glu 310	ACA Thr	TGC Cys	GCT Ala	GCA Ala	CCG Pro 315	GAA Glu	ACG Thr	AGA Arg	GGA Gly	ACG Thr 320	960
TGT Gly	GTT Gly	TTA Gly	TCA Gly	GGA Gly	CAT Gly	ACT Gly	TTC Gly	TAT Gly	GAC Gly	ACA Gly	TTC Gly	GAC Gly	AAA Gly	GCC Gly	AGA Gly	1008

Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
				325					330					335		
TAT	CAA	TTC	CAG	GGC	CCA	TGC	AAA	GAG	CTT	CTG	ATG	GCC	GCA	GAC	TGT	1056
Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Leu	Leu	Met	Ala	Ala	Asp	Cys	
			340					345					350			
TAC	TGG	AAC	ACA	TGG	GAT	GTA	AAG	GTT	TCA	CAT	AGA	GAT	GTT	GAG	TCA	1104
Tyr	Trp	Asn	Thr	Trp	Asp	Val	Lys	Val	Ser	His	Arg	Asp	Val	Glu	Ser	
		355					360					365				
TAC	ACT	GAG	GTA	GAG	AAA	GTA	ACA	ATC	AGG	AAA	CAG	TCA	ACT	GTA	GTA	1152
Tyr	Thr	Glu	Val	Glu	Lys	Val	Thr	Ile	Arg	Lys	Gln	Ser	Thr	Val	Val	
	370					375					380					
GAT	TTG	ATT	GTG	GAT	GGC	AAG	CAG	GTC	AAG	GTT	GGA	GGA	GTG	GAT	GTA	1200
Asp	Leu	Ile	Val	Asp	Gly	Lys	Gln	Val	Lys	Val	Gly	Gly	Val	Asp	Val	
385					390				395						400	
TCT	ATC	CCG	TAC	AGT	TCT	GAG	AAC	ACA	TCC	ATA	TAC	TGG	CAG	GAT	GGA	1248
Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly	
				405					410					415		
GAC	ATC	CTG	ACG	ACG	GCC	ATC	CTA	CCT	GAA	GCT	CTT	GTC	GTT	AAG	TTC	1296
Asp	Ile	Leu	Thr	Thr	Ala	Ile	Leu	Pro	Glu	Ala	Leu	Val	Val	Lys	Phe	
			420					425					430			
AAC	TTT	AAG	CAG	CTC	CTT	GTA	GTT	CAT	ATC	AGA	GAT	CCA	TTC	GAT	GGA	1344
Asn	Phe	Lys	Gln	Leu	Leu	Val	Val	His	Ile	Arg	Asp	Pro	Phe	Asp	Gly	
		435					440					445				
AAG	ACA	TGC	GGC	ATA	TGT	GGT	AAC	TAT	AAT	CAA	GAT	TCA	ACT	GAT	GAT	1392
Lys	Thr	Cys	Gly	Ile	Cys	Gly	Asn	Tyr	Asn	Gln	Asp	Ser	Thr	Asp	Asp	
	450					455					460					
TTC	TTT	GAC	GCA	GAA	GGA	GCA	TGC	GCT	CTG	ACC	CCC	AAT	CCC	CCA	GGA	1440
Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	
465					470					475					480	
TGT	ACA	GAG	GAG	CAG	AAA	CCA	GAA	GCT	GAG	CGA	CTC	TGC	AAT	AGT	CTA	1488
Cys	Thr	Glu	Glu	Gln	Lys	Pro	Glu	Ala	Glu	Arg	Leu	Cys	Asn	Ser	Leu	
				485					490					495		
TTT	GAT	AGT	TCT	ATC	GAC	GAG	AAA	TGT	AAT	GTC	TGC	TAC	AAG	CCT	GAC	1536
Phe	Asp	Ser	Ser	Ile	Asp	Glu	Lys	Cys	Asn	Val	Cys	Tyr	Lys	Pro	Asp	
			500					505					510			
CGT	ATT	GCA	CGA	TGT	ATG	TAC	GAG	TAT	TGC	CTG	AGG	GGA	CAG	CAA	GGA	1584
Arg	Ile	Ala	Arg	Cys	Met	Tyr	Glu	Tyr	Cys	Leu	Arg	Gly	Gln	Gln	Gly	
		515					520					525				
TTC	TGT	GAC	CAT	GCT	TGG	GAG	TTC	AAA	AAA	GAA	TGC	TAC	ATA	AAG	CAT	1632
Phe	Cys	Asp	His	Ala	Trp	Glu	Phe	Lys	Lys	Glu	Cys	Tyr	Ile	Lys	His	
	530					535					540					
GGA	GAC	ACT	CTA	GAA	GTA	CCA	CCT	GAA	TGC	CAA	TAA	ATGAACAAAG				1678
Gly	Asp	Thr	Leu	Glu	Val	Pro	Pro	Glu	Cys	Gln						
545					550				555							
ATACAGAAGC	TAAGACTACT	ACAGCAGAAG	ATAAAAGAGA	AGCTGTAGTT	CTTCAAAAAC											1738
AGTATATTTT	GATGTACTCA	TTGTTTACTT	ACATAAAAAT	AAATTGTTAT	TATCATAACG											1798
TAAAGAAAAA	AAAAAAAAAA	AAAAA														1822

(2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1644
- (D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)

## (x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	GAA	AAC	ATG	GAA	AAC	GAT	GAA	AAT	ATT	GTA	GTT	GGA	CCT	AAA	CCG	48
Met	Glu	Asn	Met	Glu	Asn	Asp	Glu	Asn	Ile	Val	Val	Gly	Pro	Lys	Pro	
1				5					10					15		
TTT	TAC	CCT	ATC	GAA	GAG	GGA	TCT	GCT	GGA	ACA	CAA	TTA	CGC	AAA	TAC	96
Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	Lys	Tyr	
			20					25					30			
ATG	GAG	CGA	TAT	GCA	AAA	CTT	GGC	GCA	ATT	GCT	TTT	ACA	AAT	GCA	GTT	144
Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr	Asn	Ala	Val	
		35					40					45				
ACT	GGT	GTT	GAT	TAT	TCT	TAC	GCC	GAA	TAC	TTG	GAG	AAA	TCA	TGT	TGT	192
Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu	Lys	Ser	Cys	Cys	
	50					55					60					
CTA	GGA	AAA	GCT	TTG	CAA	AAT	TAT	GGT	TTG	GTT	GTT	GAT	GGC	AGA	ATT	240
Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val	Val	Asp	Gly	Arg	Ile	
65					70				75						80	
GCG	TTA	TGC	AGT	GAA	AAC	TGT	GAA	GAA	TTT	TTT	ATT	CCT	GTA	ATA	GCC	288
Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe	Phe	Ile	Pro	Val	Ile	Ala	
				85					90					95		
GGA	CTG	TTT	ATA	GGT	GTA	GGT	GTT	GCA	CCC	ACT	AAT	GAG	ATT	TAC	ACT	336
Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala	Pro	Thr	Asn	Glu	Ile	Tyr	Thr	
			100					105					110			
TTA	CGT	GAA	CTG	GTT	CAC	AGT	TTA	GGT	ATC	TCT	AAA	CCA	ACA	ATT	GTA	384
Leu	Arg	Glu	Leu	Val	His	Ser	Leu	Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	
		115					120					125				
TTT	AGT	TCT	AAA	AAA	GGC	TTA	GAT	AAA	GTT	ATA	ACA	GTA	CAG	AAA	ACA	432
Phe	Ser	Ser	Lys	Lys	Gly	Leu	Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	
	130					135					140					
GTA	ACT	ACT	ATT	AAA	ACC	ATT	GTT	ATA	CTA	GAT	AGC	AAA	GTT	GAT	TAT	480
Val	Thr	Thr	Ile	Lys	Thr	Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	
145					150					155					160	
CGA	GGA	TAT	CAA	TGT	CTG	GAC	ACC	TTT	ATA	AAA	AGA	AAC	ACT	CCA	CCA	528
Arg	Gly	Tyr	Gln	Cys	Leu	Asp	Thr	Phe	Ile	Lys	Arg	Asn	Thr	Pro	Pro	
				165					170					175		
GGT	TTT	CAA	GCA	TCC	AGT	TTC	AAA	ACT	GTG	GAA	GTT	GAC	CGT	AAA	GAA	576

Gly	Phe	Gln	Ala	Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	
			180					185					190			
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA	624
Gln	Val	Ala	Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	
		195					200					205				
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT	672
Gly	Val	Gln	Leu	Thr	His	Glu	Asn	Thr	Val	Thr	Arg	Phe	Ser	His	Ala	
	210					215					220					
AGA	GAT	CCG	ATT	TAT	GGT	AAC	CAA	GTT	TCA	CCA	GGC	ACC	GCT	GTT	TTA	720
Arg	Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu	
225					230					235					240	
ACT	GTC	GTT	CCA	TTC	CAT	CAT	GGT	TTT	GGT	ATG	TTC	ACT	ACT	CTA	GGG	768
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	Gly	
				245					250					255		
TAT	TTA	ATT	TGT	GGT	TTT	CGT	GTT	GTA	ATG	TTA	ACA	AAA	TTC	GAT	GAA	816
Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe	Asp	Glu	
			260					265					270			
GAA	ACA	TTT	TTA	AAA	ACT	CTA	CAA	GAT	TAT	AAA	TGT	ACA	AGT	GTT	ATT	864
Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr	Ser	Val	Ile	
		275					280					285				
CTT	GTA	CCG	ACC	TTG	TTT	GCA	ATT	CTC	AAC	AAA	AGT	GAA	TTA	CTC	AAT	912
Leu	Val	Pro	Thr	Leu	Phe	Ala	Ile	Leu	Asn	Lys	Ser	Glu	Leu	Leu	Asn	
	290					295					300					
AAA	TAC	GAT	TTG	TCA	AAT	TTA	GTT	GAG	ATT	GCA	TCT	GGC	GGA	GCA	CCT	960
Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Val	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	
305					310					315					320	
TTA	TCA	AAA	GAA	GTT	GGT	GAA	GCT	GTT	GCT	AGA	CGC	TTT	AAT	CTT	CCC	1008
Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	Arg	Arg	Phe	Asn	Leu	Pro	
				325				330						335		
GGT	GTT	CGT	CAA	GGT	TAT	GGT	TTA	ACA	GAA	ACA	ACA	TCT	GCC	ATT	ATT	1056
Gly	Val	Arg	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Ile	Ile	
			340					345					350			
ATT	ACA	CCA	GAA	GGA	GAC	GAT	AAA	CCA	GGA	GCT	TCT	GGA	AAA	GTC	GTG	1104
Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys	Pro	Gly	Ala	Ser	Gly	Lys	Val	Val	
		355					360					365				
CCG	TTG	TTT	AAA	GCA	AAA	GTT	ATT	GAT	CTT	GAT	ACC	AAA	AAA	TCT	TTA	1152
Pro	Leu	Phe	Lys	Ala	Lys	Val	Ile	Asp	Leu	Asp	Thr	Lys	Lys	Ser	Leu	
	370					375					380					
GGT	CCT	AAC	AGA	CGT	GGA	GAA	GTT	TGT	GTT	AAA	GGA	CCT	ATG	CTT	ATG	1200
Gly	Pro	Asn	Arg	Arg	Gly	Glu	Val	Cys	Val	Lys	Gly	Pro	Met	Leu	Met	
385					390					395					400	
AAA	GGT	TAT	GTA	AAT	AAT	CCA	GAA	GCA	ACA	AAA	GAA	CTT	ATT	GAC	GAA	1248
Lys	Gly	Tyr	Val	Asn	Asn	Pro	Glu	Ala	Thr	Lys	Glu	Leu	Ile	Asp	Glu	
				405				410						415		
GAA	GGT	TGG	CTG	CAC	ACC	GGA	GAT	ATT	GGA	TAT	TAT	GAT	GAA	GAA	AAA	1296
Glu	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Tyr	Tyr	Asp	Glu	Glu	Lys	
			420					425					430			
CAT	TTC	TTT	ATT	GTC	GAT	CGT	TTG	AAG	TCT	TTA	ATC	AAA	TAC	AAA	GGA	1344
His	Phe	Phe	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	

	435	440	445	
TAC	CAA GTA CCA CCT GCC GAA TTA GAA TCC GTT CTT TTG CAA CAT CCA			1392
Tyr	Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro			
	450	455	460	
TCT	ATC TTT GAT GCT GGT GTT GCC GGC GTT CCT GAT CCT GTA GCT GGC			1440
Ser	Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly			
	465	470	475	480
GAG	CTT CCA GGA GCC GTT GTT GTA CTG GAA AGC GGA AAA AAT ATG ACC			1488
Glu	Leu Pro GLy Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr			
		485	490	495
GAA	AAA GAA GTA ATG GAT TAT GTT GCA AGT CAA GTT TCA AAT GCA AAA			1536
Glu	Lys Glu Val Met Asp Tyr Val Als Ser Gln Val Ser Asn Ala Lys			
		500	505	510
CGT	TTA CGT GGT GGT GTT CGT TTT GTG GAT GAA GTA CCT AAA GGT CTT			1584
Arg	Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu			
		515	520	525
ACT	GGA AAA ATT GAC GGC AGA GCA ATT AGA GAA ATC CTT AAG AAA CCA			1632
Thr	Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro			
		530	535	540
GTT	GCT AAG ATG			1644
Val	Ala Lys Met			
	545			

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1664
- (D) OTHER INFORMATION: Vargula (cypridina) luciferase

## (x) PUBLICATION INFORMATION:

JP 3-30678 Osaka (Tsuji)

(A) AUTHORS: Thompson et al.

(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

(D) VOLUME: 86

(F) PAGES: 1326-1332

(G) DATE: (1989)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG	AAG	ATA	ATA	ATT	CTG	TCT	GTT	ATA	TTG	GCC	TAC	TGT	GTC	ACC	GAC	48
Met	Lys	Ile	Ile	Ile	Leu	Ser	Val	Ile	Leu	Ala	Tyr	Cys	Val	Thr	Asp	
1				5				10					15			
AAC	TGT	CAA	GAT	GCA	TGT	CCT	GTA	GAA	GCG	GAA	CCG	CCA	TCA	AGT	ACA	96
Asn	Cys	Gln	Asp	Ala	Cys	Pro	Val	Glu	Ala	Glu	Pro	Pro	Ser	Ser	Thr	
			20				25						30			
CCA	ACA	GTT	CCA	ACT	TCT	TGT	GAA	GCT	AAA	GAA	GGA	GAA	TGT	ATA	GAT	144
Pro	Thr	Val	Pro	Thr	Ser	Cys	Glu	Ala	Lys	Glu	Gly	Glu	Cys	Ile	Asp	



35						40						45						
ACC Thr	AGA Arg 50	TGC Cys	GCA Ala	ACA Thr	TGT Cys	AAA Lys 55	CGA Arg	GAT Asp	ATA Ile	CTA Leu	TCA Ser 60	GAT Asp	GGA Gly	CTG Leu	TGT Cys	192		
GAA Glu 65	AAT Asn	AAA Lys	CCA Pro	GGG Gly	AAG Lys 70	ACA Thr	TGC Cys	TGT Cys	AGA Arg	ATG Met 75	TGC Cys	CAG Gln	TAT Tyr	GTG Val	ATT Ile 80	240		
GAA Glu	TGC Cys	AGA Arg	GTA Val	GAA Glu 85	GCA Ala	GCT Ala	GGT Gly	TAT Tyr	TTT Phe 90	AGA Arg	ACG Thr	TTT Phe	TAC Tyr	GGC Gly 95	AAA Lys	288		
AGA Arg	TTT Phe	AAT Asn	TTT Phe 100	CAG Gln	GAA Glu	CCT Pro	GGT Gly	AAA Lys 105	TAT Tyr	GTG Val	CTG Leu	GCT Ala	AGG Arg 110	GGA Gly	ACC Thr	336		
AAG Lys	GGT Gly	GGC Gly 115	GAT Asp	TGG Trp	TCT Ser	GTA Val	ACC Thr 120	CTC Leu	ACC Thr	ATG Met	GAG Glu	AAT Asn 125	CTA Leu	GAT Asp	GGA Gly	384		
CAG Gln	AAG Lys 130	GGA Gly	GCT Ala	GTG Val	CTG Leu	ACT Thr 135	AAG Lys	ACA Thr	ACA Thr	CTG Leu	GAG Glu 140	GTT Val	GCA Ala	GGA Gly	GAC Asp	432		
GTA Val 145	ATA Ile	GAC Asp	ATT Ile	ACT Thr	CAA Gln 150	GCT Ala	ACT Thr	GCA Ala	GAT Asp	CCT Pro 155	ATC Ile	ACA Thr	GTT Val	AAC Asn	GGA Gly 160	480		
GGA Gly	GCT Ala	GAC Asp	CCA Pro	GTT Val 165	ATC Ile	GCT Ala	AAC Asn	CCG Pro	TTC Phe 170	ACA Thr	ATT Ile	GGT Gly	GAG Glu	GTG Val 175	ACC Thr	528		
ATT Ile	GCT Ala	GTT Val 180	GTT Val	GAA Glu	ATA Ile	CCG Pro	GGC Gly	TTC Phe 185	AAT Asn	ATC Ile	ACA Thr	GTC Val	ATC Ile 190	GAA Glu	TTC Phe	576		
TTT Phe	AAA Lys	CTA Leu 195	ATC Ile	GTG Val	ATT Ile	GAT Asp	ATT Ile 200	CTG Leu	GGA Gly	GGA Gly	AGA Arg	TCT Ser 205	GTC Val	AGA Arg	ATT Ile	624		
GCT Ala	CCA Pro 210	GAC Asp	ACA Thr	GCA Ala	AAC Asn	AAA Lys 215	GGA Gly	CTG Leu	ATA Ile	TCT Ser	GGT Gly 220	ATC Ile	TGT Cys	GGT Gly	AAT Asn	672		
CTG Leu 225	GAG Glu	ATG Met	AAT Asn	GAC Asp	GCT Ala 230	GAT Asp	GAC Asp	TTT Phe	ACT Thr	ACA Thr 235	GAT Asp	GCA Ala	GAT Asp	CAG Gln	CTG Leu 240	720		
GCG Ala	ATC Ile	CAA Gln	CCC Pro	AAC Asn 245	ATA Ile	AAC Asn	AAA Lys	GAG Glu	TTC Phe 250	GAC Asp	GGC Gly	TGC Cys	CCA Pro	TTC Phe 255	TAT Tyr	768		
GGC Gly	AAT Asn	CCT Pro	TCT Ser 260	GAT Asp	ATC Ile	GAA Glu	TAC Tyr	TGC Cys 265	AAA Lys	GGT Gly	CTG Leu	ATG Met	GAG Glu 270	CCA Pro	TAC Tyr	816		
AGA Arg	GCT Ala	GTA Val 275	TGT Cys	CGT Arg	AAC Asn	AAT Asn	ATC Ile 280	AAC Asn	TTC Phe	TAC Tyr	TAT Tyr	TAC Tyr 285	ACT Thr	CTA Leu	TCC Ser	864		
TGT Cys	GCC Ala 290	TTC Phe	GCT Ala	TAC Tyr	TGT Cys	ATG Met 295	GGA Gly	GGA Gly	GAA Glu	GAA Glu	AGA Arg 300	GCT Ala	AAA Lys	CAC His	GTC Val	912		

CTT TTC GAC TAT GTT GAG ACA TGC GCT GCG CCG GAA ACG AGA GGA ACG 960  
 Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr  
 305 310 315 320

TGT GTT TTA TCA GGA CAT ACT TTC TAT GAC ACA TTC GAC AAA GCA AGA 1008  
 Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg  
 325 330 335

TAT CAA TTC CAG GGC CCA TGC AAG GAG ATT CTG ATG GCC GCA GAC TGT 1056  
 Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys  
 340 345 350

TAC TGG AAC ACA TGG GAT GTA AAG GTT TCA CAT AGA GAC GTC GAA TCA 1104  
 Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser  
 355 360 365

TAC ACT GAG GTA GAG AAA GTA ACA ATC AGG AAA CAG TCA ACT GTA GTA 1152  
 Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val  
 370 375 380

GAT CTC ATT GTG GAT GGC AAG CAG GTC AAG GTT GGA GGA GTG GAT GTA 1200  
 Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val  
 385 390 395 400

TCT ATC CCG TAC AGC TCT GAG AAC ACT TCC ATA TAC TGG CAG GAT GGA 1248  
 Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly  
 405 410 415

GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC 1296  
 Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe  
 420 425 430

AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GCA 1344  
 Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Ala  
 435 440 445

AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT 1392  
 Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp  
 450 455 460

TTC TTT GAC GCA GAA GGA GCA TGC GCT CTA ACC CCC AAC CCC CCA GGA 1440  
 Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly  
 465 470 475 480

TGT ACA GAG GAA CAG AAA CCA GAA GCT GAG CGA CTT TGC AAT AAT CTC 1488  
 Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu  
 485 490 495

TTT GAT TCT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC 1536  
 Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp  
 500 505 510

CGG ATT GCC CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAA CAA GGA 1584  
 Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly  
 515 520 525

TTT TGT GAC CAT GCT TGG GAG TTC AAG AAA GAA TGC TAC ATA AAA CAT 1632  
 Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His  
 530 535 540

GGA GAC ACT CTA GAA GTA CCA CCT GAA TGT CAA TAA ACGTACAAAG 1678  
 Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln  
 545 550 555

ATACAGAAGC TAAGGCTACT ACAGCAGAAG ATAAAAAGA AACTGTAGTT CCTTCAAAAA 1738  
 CCGTGTATTT TATGTACTCA TTGTTTAATT AGAGCAAAAT AAATTGTTAT TATCATAACT 1798

TAAACTAAAA AAAAAAAAAA AA

1820

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 115...702

(D) OTHER INFORMATION: apoaeguorin-encoding gene

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,093,240

(A) AUTHORS: Inouye et al.

(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

(D) VOLUME: 82

(F) PAGES: 3154-3158

(G) DATE: (1985)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGAATGCAA TTCATCTTTG CATCAAAGAA      60
TTACATCAAA TCTCTAGTTG ATCAACTAAA TTGTCTCGAC AACAACAAGC AAAC ATG      117
                                     Met
                                     1

ACA AGC AAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC CCA      165
Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro
                    5                      10                      15

AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC AAC      213
Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn
                20                      25                      30

CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT GAT      261
His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp
                35                      40                      45

ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA CAC      309
Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His
                50                      55                      60

AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT      357
Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly
                    70                      75                      80

GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG GCT      405
Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala
                    85                      90                      95

ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC CGT      453
Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg
                100                      105                      110

```

```

ATA TGG GGT GAT GCT TTG TTT GAT ATC GTT GAC AAA GAT CAA AAT GGA      501
Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly
      115                      120                      125

GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT ATC      549
Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile
      130                      135                      140                      145

ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT      597
Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile
      150                      155                      160

GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA      645
Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu
      165                      170                      175

GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA      693
Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly
      180                      185                      190

GCT GTC CCC TAAGAAGCTC TACGGTGGTG ATGCACCCTA GGAAGATGAT GTGATTTTGA 752
Ala Val Pro
      195

ATAAAACACT GATGAATTCA ATCAAAATTT TCCAAATTTT TGAACGATTT CAATCGTTTG      812
TGTTGATTTT TGTAATTAGG AACAGATTAA ATCGAATGAT TAGTTGTTTT TTTAATCAAC      872
AGAACTTACA AATCGAAAAA GTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      932
AAAAAAAAAA AAAAAAAAAA AAAAAA

```

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...588
- (D) OTHER INFORMATION: Recombinant Aequorin AEQ1

## (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
- (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
- (C) JOURNAL: Biochemistry
- (D) VOLUME: 26
- (F) PAGES: 1326-1332
- (G) DATE: 1987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
      1                      5                      10                      15

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC      96

```

Pro	Lys	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val		
			20					25					30				
AAC	CAC	AAT	GGA	AGG	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	144	
Asn	His	Asn	Gly	Arg	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser		
		35					40				45						
GAT	ATT	GTT	ATA	AAC	AAT	CTT	GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	192	
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg		
	50					55					60						
CAC	AAA	GAT	GCT	GTA	GAA	GCC	TTC	TTC	GGA	GGA	GCT	GGA	ATG	AAA	TAT	240	
His	Lys	Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr		
65					70				75					80			
GGT	GTA	GAA	ACT	GAA	TGG	CCT	GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	288	
Gly	Val	Glu	Thr	Glu	Trp	Pro	Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu		
			85					90						95			
GCT	TCC	GAG	GAA	TTG	AAA	AGG	TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	336	
Ala	Ser	Glu	Glu	Leu	Lys	Arg	Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile		
			100					105					110				
CGT	TTA	TGG	GGT	GAT	GCA	TTG	TTC	GAT	ATC	ATT	GAC	AAA	GAC	CAA	AAT	384	
Arg	Leu	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn		
		115					120					125					
GGA	GCT	ATT	TCA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	TCT	GAT	GGC	432	
Gly	Ala	Ile	Ser	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Asp	Gly		
	130					135					140						
ATC	ATC	CAA	TCG	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	480	
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp		
145					150					155					160		
ATT	GAT	GAA	AGT	GGA	CAG	CTC	GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	528	
Ile	Asp	Glu	Ser	Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His		
				165					170					175			
TTA	GGA	TTT	TGG	TAC	ACC	ATG	GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	576	
Leu	Gly	Phe	Trp	Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly		
			180					185					190				
GGA	GCT	GTC	CCC	TAA												591	
Gly	Ala	Val	Pro	*													
		195															

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...588

## (D) OTHER INFORMATION: Recombinant Aequorin AEQ2

## (x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.  
 (B) TITLE: Sequence Comparisons of Complementary  
 DNAs Encoding Aequorin Isotypes  
 (C) JOURNAL: Biochemistry  
 (D) VOLUME: 26  
 (F) PAGES: 1326-1332  
 (G) DATE: 1987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn	
1 5 10 15	
CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	
CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT	384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn	
115 120 125	
GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT	432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly	
130 135 140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC TAA	591
Gly Ala Val Pro *	
195	

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (A) NAME/KEY: Coding Sequence

## (B) LOCATION: 1...588

## (D) OTHER INFORMATION: Recombinant Aequorin AEQ3

## (x) PUBLICATION INFORMATION:

## (A) AUTHORS: Prasher et al.

## (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes

## (C) JOURNAL: Biochemistry

## (D) VOLUME: 26

## (F) PAGES: 1326-1332

## (G) DATE: 1987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	TCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AGA	TGG	ATT	GGA	CGA	CAC	AAG	CAT	ATG	TTC	AAT	TTC	CTT	GAT	GTC	96
Pro	Arg	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20					25					30			
AAC	CAC	AAT	GGA	AAA	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCA	TCT	144
Asn	His	Asn	Gly	Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
		35					40					45				
GAT	ATT	GTC	ATC	AAT	AAC	CTT	GGA	GCA	ACA	CCT	GAG	CAA	GCC	AAA	CGA	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
	50					55					60					
CAC	AAA	GAT	GCT	GTA	GGA	GAC	TTC	TTC	GGA	GGA	GCT	GGA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Gly	Asp	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	
	65				70				75					80		
GGT	GTG	GAA	ACT	GAT	TGG	CCT	GCA	TAC	ATT	GAA	GGA	TGG	AAA	AAA	TTG	288
Gly	Val	Glu	Thr	Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	
			85						90					95		
GCT	ACT	GAT	GAA	TTG	GAG	AAA	TAC	GCC	AAA	AAC	GAA	CCA	ACG	CTC	ATC	336
Ala	Thr	Asp	Glu	Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	
			100					105					110			
CGT	ATA	TGG	GGT	GAT	GCT	TTG	TTC	GAT	ATC	GTT	GAC	AAA	GAT	CAA	AAT	384
Arg	Ile	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	
		115					120					125				
GGA	GCC	ATT	ACA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	GCT	GCT	GGT	432
Gly	Ala	Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	

130		135		140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480				
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp					
145 150 155 160					
ATT GAT GAA AAT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528				
Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His					
165 170 175					
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576				
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly					
180 185 190					
GGA GCT GTC CCC TAA	591				
Gly Ala Val Pro *					
195					

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (A) NAME/KEY: Coding Sequence

## (B) LOCATION: 1...567

## (D) OTHER INFORMATION: Aequorin photoprotein

## (x) PUBLICATION INFORMATION:

## (A) AUTHORS: Charbonneau et al.

## (B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin

## (C) JOURNAL: Am. Chem. Soc.

## (D) VOLUME: 24

## (E) ISSUE: 24

## (F) PAGES: 6762-6771

## (G) DATE: 1985

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC	48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His	
1 5 10 15	
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT	96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser	
20 25 30	
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT	144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Asn Asn Leu	
35 40 45	
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC	192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala	



50	55	60	
TTC TTC GGA GGA GCT GCA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT			240
Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro			
65	70	75	80
GAA TAC ATC GAA GGA TGG AAA AGA CTG GCT TCC GAG GAA TTG AAA AGG			288
Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg			
	85	90	95
TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG			336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu			
	100	105	110
TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT TCA CTG GAT GAA			384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu			
	115	120	125
TGG AAA GCA TAC ACC AAA TCT GCT GGC ATC ATC CAA TCG TCA GAA GAT			432
Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp			
	130	135	140
TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC			480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu			
	145	150	155
GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG			528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met			
	165	170	175
GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA GCT GTC CCC			567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro			
	180	185	

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (A) NAME/KEY: Coding Sequence

## (B) LOCATION: 1...588

(D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activity

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

## (K) RELEVANT RESIDUES IN SEQ ID NO: 10:

Asp 124 changed to Ser

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	

1	5	10	15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC				96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	20	25	30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC				144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	35	40	45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT				192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	50	55	60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT				240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	65	70	75	80
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG				288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	85	90	95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT				336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	100	105	110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT				384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	115	120	125	
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC				432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly	130	135	140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT				480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	145	150	155	160
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT				528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	165	170	175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT				576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	180	185	190	
GGA GCT GTC CCC				588
Gly Ala Val Pro	195			

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...588  
 (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant  
 w/increased biolum. activity

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 11:  
 Glu 135 changed to Ser

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GGA GCT ATT TCA CTG GAT TCA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (A) NAME/KEY: Coding Sequence

## (B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant site-directed  
Aequorin mutant w/increased biolum. activity

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AAA	TGG	ATT	GGA	CGA	CAC	AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	96
Pro	Lys	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20					25					30			
AAC	CAC	AAT	GGA	AGG	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	144
Asn	His	Asn	Gly	Arg	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
		35					40					45				
GAT	ATT	GTT	ATA	AAC	AAT	CTT	GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
	50					55					60					
CAC	AAA	GAT	GCT	GTA	GAA	GCC	TTC	TTC	GGA	GGA	GCT	GCA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Ala	Met	Lys	Tyr	
65					70				75						80	
GGT	GTA	GAA	ACT	GAA	TGG	CCT	GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	288
Gly	Val	Glu	Thr	Glu	Trp	Pro	Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	
				85					90					95		
GCT	TCC	GAG	GAA	TTG	AAA	AGG	TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	336
Ala	Ser	Glu	Glu	Leu	Lys	Arg	Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	
			100					105					110			
CGT	TTA	TGG	GGT	GAT	GCA	TTG	TTC	GAT	ATC	ATT	TCC	AAA	GAC	CAA	AAT	384
Arg	Leu	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Ile	Ser	Lys	Asp	Gln	Asn	
	115						120					125				
GCA	GCT	ATT	TCA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	TCT	GCT	GGC	432
Ala	Ala	Ile	Ser	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Ala	Gly	
	130					135					140					
ATC	ATC	CAA	TCG	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	480
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	
145					150				155						160	

ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...567  
 (D) OTHER INFORMATION: Recombinant apoaeguorin (AQUALITE®)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC	48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His	
1 5 10 15	
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT	96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser	
20 25 30	
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT	144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu	
35 40 45	
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC	192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala	
50 55 60	
TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT	240
Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro	
65 70 75 80	
GAA TAC ATC GAA GGA TGG AAA AAA CTG GCT TCC GAG GAA TTG AAA AGG	288
Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg	
85 90 95	
TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG	336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu	
100 105 110	
TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT CTG TCA GAT GAA	384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu	
115 120 125	
TGG AAA GCA TAC ACC AAA TCT GAT GGC ATC ATC CAA TCG TCA GAA GAT	432
Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Gln Ser Ser Glu Asp	
130 135 140	

TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	ATT	GAT	GAA	AGT	GGA	CAG	CTC	480
Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser	Gly	Gln	Leu	
145					150					155					160	
GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	TTA	GGA	TTT	TGG	TAC	ACC	ATG	528
Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp	Tyr	Thr	Met	
				165					170					175		
GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	GGA	GCT	GTC	CCC				567
Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly	Ala	Val	Pro				
			180					185								

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,484,723

## (ix) FEATURE:

(D) OTHER INFORMATION: *Vibrio fisheri* Flavin reductase

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Pro	Ile	Asn	Cys	Lys	Val	Lys	Ser	Ile	Glu	Pro	Leu	Ala	Cys	Asn	
1				5					10					15		
Thr	Phe	Arg	Ile	Leu	Leu	His	Pro	Glu	Gln	Pro	Val	Ala	Phe	Lys	Ala	
			20					25					30			
Gly	Gln	Tyr	Leu	Thr	Val	Val	Met	Gly	Glu	Lys	Asp	Lys	Arg	Pro	Phe	
		35					40					45				
Ser	Ile	Ala	Ser	Ser	Pro	Cys	Arg	His	Glu	Gly	Glu	Ile	Glu	Leu	His	
50						55					60					
Ile	Gly	Ala	Ala	Glu	His	Asn	Ala	Tyr	Ala	Gly	Glu	Val	Val	Glu	Ser	
65					70					75					80	
Met	Lys	Ser	Ala	Leu	Glu	Thr	Gly	Gly	Asp	Ile	Leu	Ile	Asp	Ala	Pro	
				85					90					95		
His	Gly	Glu	Ala	Trp	Ile	Arg	Glu	Asp	Ser	Asp	Arg	Ser	Met	Leu	Leu	
			100					105					110			
Ile	Ala	Gly	Gly	Thr	Gly	Phe	Ser	Tyr	Val	Arg	Ser	Ile	Leu	Asp	His	
		115					120					125				
Cys	Ile	Ser	Gln	Gln	Ile	Gln	Lys	Pro	Ile	Tyr	Leu	Tyr	Trp	Gly	Gly	
130						135					140					
Arg	Asp	Glu	Cys	Gln	Leu	Tyr	Ala	Lys	Ala	Glu	Leu	Glu	Ser	Ile	Ala	
145					150					155					160	
Gln	Ala	His	Ser	His	Ile	Thr	Phe	Val	Pro	Val	Val	Glu	Lys	Ser	Glu	
				165					170					175		
Gly	Trp	Thr	Gly	Lys	Thr	Gly	Asn	Val	Leu	Glu	Ala	Val	Lys	Ala	Asp	

180					185					190					
Phe	Asn	Ser	Leu	Ala	Asp	Met	Asp	Ile	Tyr	Ile	Ala	Gly	Arg	Phe	Glu
		195					200					205			
Met	Ala	Gly	Ala	Ala	Arg	Glu	Gln	Phe	Thr	Thr	Glu	Lys	Gln	Ala	Lys
	210					215					220				
Lys	Glu	Gln	Leu	Phe	Gly	Asp	Ala	Phe	Ala	Phe	Ile				
225					230					235					